

Indiana University-Purdue University Indianapolis

Department of Mathematical Sciences

STATISTICS SEMINAR

12:15pm—1:15pm, Tuesday, April 04, 2023

Zoom Meeting: Meeting ID: 845 0989 4694

Speaker: Yuehua Cui

*Department of Statistics and Probability,
Michigan State University*

Title: Mendelian randomization for causal inference with longitudinal traits

Abstract:

Mendelian randomization (MR) uses genetic variants as instrument variables to determine whether an observational association between an exposure and an outcome is causal. The use of Mendelian Randomization reduces regression bias and provides reliable estimate of the likely underlying causal relationship between an exposure and a disease outcome. Most current Mendelian randomization methods are focused on cross-sectional phenotypic traits. Longitudinal studies track the same individual at different time points and have a number of advantages over cross-sectional studies. Motivated by a real study to evaluate the causal effect of hormone level on eating behavior, we propose two MR models to investigate the causal effects in a longitudinal study. In the first model, we assume the current exposure affects the current outcome. In the second model, we assume that the past and/or current exposures contribute to the current outcome. The delayed causal effect is determined by data through a variable selection algorithm. Point-wise and simultaneous testing are developed to assess the existence of causal effects. The utility of the method was illustrated via simulation studies and an application to an eating behavior dataset.

Bio:

Dr. Yuehua Cui is a full Professor in the Department of Statistics and Probability at Michigan State University. He got his PhD in Statistics from University of Florida in 2005. Dr. Cui's research interests focus on statistical genetics including genetic association study, (e)QTL mapping, gene-gene and gene-environment interactions; high-dimensional mediation analysis; statistical genomics including microarray data analysis, RNA-Seq and Chip-Seq data analysis, clustering,

gene set enrichment analysis and gene network inference; longitudinal data analysis, functional data analysis, mixture model; as well as statistical applications in biological sciences.